

- C¹
- c) a biologically-active fragment of the amino acid sequence of SEQ ID NO:1, and
 - d) an antigenically-active fragment of the amino acid sequence of SEQ ID NO:1.

C²

18. (Once Amended.) The method of claim [17] 20, wherein before hybridization, the [nucleic acid material of the biological sample] target polynucleotide is amplified by the polymerase chain reaction.

Please add the following new claims:

- Sub D1
19. An isolated polynucleotide selected from the group consisting of:
- a) a polynucleotide sequence of SEQ ID NO:2,
 - b) a naturally-occurring polynucleotide sequence having at least 90% sequence identity to the sequence of SEQ ID NO:2 and
 - b) a polynucleotide sequence complementary to a) or b).

C³

20. A method of detecting a target polynucleotide in a sample, said target polynucleotide having the sequence of a polynucleotide of claim 19, comprising

hybridizing the sample with a probe comprising at least 16 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and

detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

Sub G3

21. A method of claim 20, wherein the probe comprises at least 30 contiguous nucleotides.

22. A method of claim 20, wherein the probe comprises at least 60 contiguous nucleotides.